

QUERY CONTROL FORM

PA - IDC

RTIS USE ONLY

Application No. 09/674,330
 Examiner-GAU Hutton - 1652
KERL

Prepared by Lis Stone
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JACKET

a. Serial No.	f. Foreign Priority	k. Print Claim(s)	p. PTO-1449
b. Applicant(s)	g. Disclaimer	l. Print Fig.	q. PTOL-85b
c. Continuing Data	h. Microfiche Appendix	m. Searched Column	r. Abstract
d. PCT	i. Title	n. PTO-270/328	s. Sheets/Figs
e. Domestic Priority	j. Claims Allowed	o. PTO-892	t. Other

SPECIFICATION

- a. Page Missing
- b. Text Continuity
- c. Holes through Data
- d. Other Missing Text
- e. Illegible Text
- f. Duplicate Text
- g. Brief Description
- h. Sequence Listing
- i. Appendix
- j. Amendments
- k. Other

MESSAGE

Page 32, lines 18, 19 and 21, the amendments
 are illegible. Copy provided for reference.

CLAIMS

- a. Claim(s) Missing
- b. Improper Dependency
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09/674,330

Next, isolation and cloning of full-length cDNA using the fragment of the A55 clone (hereafter A55 SST fragment cDNA) was attempted. It was confirmed that the A55 SST fragment cDNA contains a signal peptide by comparison with known peptides which have signal peptides in view of function and structure.

Example 4

Cloning and sequencing of a full-length cDNA of A55

Phage particles of a cDNA library of mouse day 13 embryonic heart (uni-ZAP XR, Stratagene) were transfected into *E. coli* XL1-Blue MRF* host cells (Stratagene). One million plaques were obtained and transferred to nylon membranes. The membranes were hybridized with 32P-labeled mouse A55 SST fragment cDNA as a probe. Many positive plaques were obtained.

From one positive plaque, the phage particles containing a cloned insert were prepared, and were subjected to conversion into phagemid particles (pBluescript SK(-)) by co-infection of *E. coli* XL1-Blue MRF* host cells (Stratagene) with ExAssist helper phage (Stratagene). The phagemid particles were transfected to *E. coli* DH5 α . The plasmids were prepared from the obtained transformants.

Nucleotide sequence of the 5'-end of the cDNA were determined to confirm the existence of the sequences of the SST fragment cDNA. Full-length sequencing was then performed to obtain a cDNA encoding SEQ ID NO:3.

An open reading frame was determined. The translation region for the amino acid sequence is shown in SEQ ID NO: 1 and the deduced full-length amino acid sequence is shown in SEQ ID NO: 3. A mature version of the protein was deduced to be 425 amino acids, as SEQ ID NO: 2 (144...1418) or 423 amino acids as shown in SEQ ID NO. 4. The translated region